

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGAGGAGCAGCTCCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCCGC
CTGGAGGCACAGGCCATGAGGGGGCTCTCAGGAGGTGCTGTGTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCAGC
GGGACCCCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCAGC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGTCTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGTCTGGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACCTC
TTCAGCAGCTCGGCCCATCGACTCCCTGAGCGAGCAGATTTCTTCTGGAGGAGCAGCT
GGGGTCTCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTGGACTGAGCCCC
TCACGCCGCCCTGCAGCCCCCATGCCCTGCCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTCTTCTCCTCCTCCCTTCTCTCGGGAG
GCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCTTGGCTACC
CCCACCTTGGTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC
GAGTCTCCTGTCTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGTGCCTGACCCCCAGCACATAAAAAATGAAACGTG

007626-10150

FIGURE 217

MRGSQEVLLMWLLVLA VGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

097829-10404

FIGURE 218

GGTTGCCACAGCTGGTTTAAAGGCCCCGACCACTGGGGCCCCCTTGTGAGGAGGAGACAGCTCCCCGGCCCCGGGAG
 GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCCTGGGACGGTCCGTTTCTGCGCTGACGTGCCGGCCG
 AGTTGGGTCTCCGCTGTTTACGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGCCGGTTTATCGGAGG
 AGATTGCTCTTCAGGGCTAGCAATTGGACTTTTGATGATGTTGACCCAGCGGCAGGAATAGCAGGCCAACCTGAT
 TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTGCTAAATCGCAAAACCCATTTTGGAGCAGGAATCCAATCA
 TGTCTGTGATGTTGGTGAGAAAGAGGTGACACGGAATGGGAGAACTCCAGGCAGGAACACCTTTTGTCTGTG
 ATGGCCCGCTCATGATGGCCCGGCAAAAGGGCATTTTCTACCTGACCCTTTTCTCATCTCTGGGACATGTACAC
 TCTTCTTCGCTTTGAGTCCGCTACCTGGCTGTTGAGCTGTCTCCTGCCATCCCTGTATTGTCTGCCATGCTCT
 TCCTTTCTCCATGGCTACACTGTTGAGGACCACTTCAGTGACCTGGAGTATTCTCGGGCTACACAGATG
 AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGGGTGCGGTGCCAGGGCCAGCGACACCGCTCGTA
 TCAAGAATTTCCAGATAAACCAACAGATTGTGAACTGAAATACCTGTACACATGCAAGATCTTCCGGCTCCCC
 GGGCTCCCCATTGACGACATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTTGTG
 TTGGAAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTCTCTCTCCCTCCTCACAACTCTATGCTTCGCT
 TCAACATCGTCTATGTGGCCCTCAAATCTTGAAATTTGGCTCTTGGAGACATTGAAAGAACTCCTGGAACTG
 TTCTAGAAGTCTCATTGTCTTCTTACACTCTGGTCCGTGTTGGGACTGACTGGATTTCACTACTTCTCTGCTG
 CTCTCAACAGACACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCTCCAGAACTCCTACAGCC
 ATGGCAATATTGTGAAGAACTGCTGTGAAGTGTCTGTGGCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGT
 TTTTGGCACTGGAGGAAAGTGAAGTGCACCTCCAGTACTCAAGAGACAGTAGCAGCTCTTGCCACAGAGCC
 CAGCCCCCAGAGAACCTGAACTCAAATGAGATGCCGAGGACAGCAGCACTCCCGAAGAGATGCCACTCCAG
 AGCCCCCAGAGCCACCAAGGAGGCTCAGTCAAGCTGAGAAGTACGCTATCTATGGAAGAGACTTTTGTGTTGTT
 TAATTAGGGCTATGAGAGTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAACTGCTCTTTTAACT
 GTTTTCTTTGCTTTAGTACCCACAGTTCACACATGGCATTCTTCTGTGCAAGCTTTTAAATTTCTGAACT
 CAGGCACTGGCAGAGATGTCACTCACTCTGATTAAGTAAATGGGTCTCTGGGCCCTGGCACTGGTCTCT
 CCATGCGCTCAGCCACAGGCTCCCCCTGGACCCCTCTCTCCCTCCAGATCCAGCCCTCTGCTTGGGGTCACT
 TGGTCTCATCTGGGGCTAAAGTTTGTGAGACTGGCTCAAATCCTCCCAAGCTGTGCAAGTGTGAGTCCAG
 GCGAGTACAGAGACCTCTGGCCAGGGGATCTAACTGGGTCTTGGGGTCTCAGGACTGAAGAGGAGGAGAG
 TGGGGTCAAGATTTCTCTGGCCACCAAGTGCAGCATTGCCACAAATCCTTTAGGAATGGGACAGGTACCT
 TCCACTTGTGTANN
 CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCACTTTTCTCTCAGAGGAAGCCGAGTGCTCACTTAAAC
 ACTATCCCTCAGACTCCCTGTGTGAGGCTGCAGAGGCCCTGAATGCACAAAATGGGAAACCAAGGCACAGAG
 GCTCTCTCTCTCTCTCTCTCCCCGATGTACCTCAAAAAAATAAATGCTAACCAAGTCTCTCACTTAAAGCT
 CGGCTGAGTGAAGGAAAGCCAGCACTGCTGCCCTCTGGGTAACTCACCTAAGGCTCGGCCCACTCTGGCT
 ATGTTAAACACACTGGGGCTTCTCCAAGCCCGCTCTTCCAGCACTTCCACCGGACAGATCCAGAGGCCACTT
 CACCTTGGGGTGGGCTGTGGCCCCAGTCACTCTGCTCAGGACCTCTCTATTTCAGGGAAGAGATTATGT
 ATTATATGTGGCTATATTTCTAGAGCACTGTGTTTTCTCTTCTAAGCCAGGCTCTGCTGTGAGTACCTTAT
 CGGTTGGGGGATGTAAACCGGAACCTTTTCACTATTTTGAAGCGATTAAACTGTGCTAATGCA

09078295.101571